



46

SEQUENCE LISTING

<110> Yanofsky, Martin F.
Liljegren, Sarah
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The Regents of the University of California

<120> Selective Control of Lignin Biosynthesis in Transgenic Plants

<130> 19452A-000940US

<140> US 09/981,087

<141> 2001-10-15

<150> US 60/090,649

<151> 1998-06-25

<150> US 09/339,998

<151> 1999-06-25

<160> 25

<170> PatentIn Ver. 2.1

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<211> 1062

<212> DNA

<213> Arabidopsis sp.

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<221> CDS

<222> (101)..(829)

<223> AGAMOUS-LIKE 8 (AGL8)

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Met Gly Arg Gly Arg
1 5

gtt cag ctg aag agg ata gag aac aag atc aat agg caa gtt act ttc 163
Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe
10 15 20

tca aag aga agg tct ggt ttg ctc aag aaa gct cat gag atc tct gtt 211
Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala His Glu Ile Ser Val
25 30 35

ctc tgc gat gct gag gtt gct ctc atc gtc ttc tct tcc aaa ggc aaa 259
Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe Ser Ser Lys Gly Lys
40 45 50

ctc ttc gaa tat tcc acc gac tct tgc atg gag agg ata ctt gaa cgc 307
Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu Arg Ile Leu Glu Arg
55 60 65

tat gat cgc tat tta tat tca gac aaa caa ctt gtt ggc cga gac gtt 355
Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu Val Gly Arg Asp Val
70 75 80 85

tca caa agt gaa aat tgg gtt cta gaa cat gct aag ctc aag gca aga 403
 Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala Lys Leu Lys Ala Arg
 90 95 100

gtt gag gta ctt gag aag aac aaa agg aat ttt atg ggg gaa gat ctt 451
 Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe Met Gly Glu Asp Leu
 105 110 115

gat tcg ttg agc ttg aag gag ctc caa agc ttg gag cat cag ctc gat 499
 Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu Glu His Gln Leu Asp
 120 125 130

gca gct atc aag agc att agg tca aga aag aac caa gct atg ttc gaa 547
 Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn Gln Ala Met Phe Glu
 135 140 145

tcc ata tct gcg ctc cag aag aag gat aaa gcc ttg caa gat cac aac 595
 Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala Leu Gln Asp His Asn
 150 155 160 165

aat tcg ctt ctc aaa aag att aag gag agg gag aag aaa acg ggt cag 643
 Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu Lys Lys Thr Gly Gln
 170 175 180

caa gaa gga caa tta gtc caa tgc tcc aac tct tct tca gtt ctt ctg 691
 Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser Ser Ser Val Leu Leu
 185 190 195

cct caa tac tgc gta acc tcc tcc aga gat ggc ttt gtg gag aga gtt 739
 Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly Phe Val Glu Arg Val
 200 205 210

ggg gga gag aac ggt ggt gca tcg tcg ttg acg gaa cca aac tct ctg 787
 Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr Glu Pro Asn Ser Leu
 215 220 225

ctt ccg gct tgg atg tta cgt cct acc act acg aac gag tag 829
 Leu Pro Ala Trp Met Leu Arg Pro Thr Thr Asn Glu
 230 235 240

aactatctca ctctttataa tataatgata atataattaa tgtttaatat tttcataaca 889

ttcagcatttt ttttggtgac ttatactcat tattaataacc gatatgtttt agctagtcac 949

attatatgta tgatggaact ccgttgctga gacgtatgta cgtaagctat cattagattc 1009

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<213> Arabidopsis sp.

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His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe
 35 40 45

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Ser Ser Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu
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Arg Ile Leu Glu Arg Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu
 65      70      75      80
Val Gly Arg Asp Val Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala
      85      90      95
Lys Leu Lys Ala Arg Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe
      100      105      110
Met Gly Glu Asp Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu
      115      120      125
Glu His Gln Leu Asp Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn
      130      135      140
Gln Ala Met Phe Glu Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala
145      150      155      160
Leu Gln Asp His Asn Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu
      165      170      175
Lys Lys Thr Gly Gln Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser
      180      185      190
Ser Ser Val Leu Leu Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly
      195      200      205
Phe Val Glu Arg Val Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr
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Asn Glu

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<222> (7)..(753)

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aaa cta ggg aga ggg aaa ata gag ata aag agg ata gag aac aca aca      96
Lys Leu Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr
    15              20              25              30

aat cgt caa gtt act ttc tgc aaa cga cgc aat ggt ctt ctc aag aaa      144
Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys
        35              40              45

gct tat gaa ctc tct gtc ttg tgt gat gcc gaa gtt gcc ctc gtc atc      192
Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile
        50              55              60

ttc tcc act cgt ggc cgt ctc tat gag tac gcc aac aac agt gtg agg      240
Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg
        65              70              75

ggg aca att gaa agg tac aag aaa gct tgt tcc gat gcc gtc aac cct      288
Gly Thr Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro
    80              85              90

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cct tcc gtc acc gaa gct aat act cag tac tat cag caa gaa gcc tct 336
 Pro Ser Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser
 95 100 105 110

 aag ctt cgg agg cag att cga gat att cag aat tca aat agg cat att 384
 Lys Leu Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile
 115 120 125

 gtt ggg gaa tca ctt ggt tcc ttg aac ttc aag gaa ctc aaa aac cta 432
 Val Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu
 130 135 140

 gaa gga cgt ctt gaa aaa gga atc agc cgt gtc cgc tcc aaa aag aat 480
 Glu Gly Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn
 145 150 155

 gag ctg tta gtg gca gag ata gag tat atg cag aag agg gaa atg gag 528
 Glu Leu Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu
 160 165 170

 ttg caa cac aat aac atg tac ctg cga gca aag ata gcc gaa ggc gcc 576
 Leu Gln His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala
 175 180 185 190

 aga ttg aat ccg gac cag cag gaa tcg agt gtg ata caa ggg acg aca 624
 Arg Leu Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr
 195 200 205

 gtt tac gaa tcc ggt gta tct tct cat gac cag tcg cag cat tat aat 672
 Val Tyr Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn
 210 215 220

 cgg aac tat att ccg gtg aac ctt ctt gaa ccg aat cag caa ttc tcc 720
 Arg Asn Tyr Ile Pro Val Asn Leu Leu Glu Pro Asn Gln Gln Phe Ser
 225 230 235

 ggc caa gac caa cct cct ctt caa ctt gtg taa ctcaaaacat gataacttgt 773
 Gly Gln Asp Gln Pro Pro Leu Gln Leu Val
 240 245

 ttcttccccct cataacgatt aagagagaga cgagagagtt catttttatat ttataacgcg 833

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 tca 896

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 35 40 45
 Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile Phe Ser
 50 55 60

Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr
 65 70 75 80
 Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro Pro Ser
 85 90 95
 Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser Lys Leu
 100 105 110
 Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile Val Gly
 115 120 125
 Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu Glu Gly
 130 135 140
 Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn Glu Leu
 145 150 155 160
 Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu Leu Gln
 165 170 175
 His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala Arg Leu
 180 185 190
 Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr Val Tyr
 195 200 205
 Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn Arg Asn
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 Asp Gln Pro Pro Leu Gln Leu Val
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<222> (78)..(818)

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 1 5 10

agc agc aag aag ata ggg aga ggg aag ata gag ata aag agg ata gag 158
 Ser Ser Lys Lys Ile Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu
 15 20 25

aac act acg aat cgt caa gtc act ttc tgc aaa cga cgc aat ggt tta 206
 Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu
 30 35 40

ctc aag aaa gct tat gag ctc tct gtc ttg tgt gac gct gag gtt gct 254
 Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala
 45 50 55

ctt gtc atc ttc tcc act cga ggc cgt ctc tac gag tac gcc aac aac 302
 Leu Val Ile Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn
 60 65 70 75

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                        80                        85                        90

gtt aac cct ccg acc atc acc gaa gct aat act cag tac tat cag caa 398
Val Asn Pro Pro Thr Ile Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln
                        95                        100                        105

gag gcg tct aaa ctc cgg aga cag att cgg gac att cag aat ttg aac 446
Glu Ala Ser Lys Leu Arg Arg Gln Ile Arg Asp Ile Gln Asn Leu Asn
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aga cac att ctt ggt gaa tct ctt ggt tcc ttg aac ttt aag gaa ctc 494
Arg His Ile Leu Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu
                        125                        130                        135

aag aac ctt gaa agt agg ctt gag aaa gga atc agt cgt gtc cga tcc 542
Lys Asn Leu Glu Ser Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser
140                        145                        150                        155

aag aag cac gag atg tta gtt gca gag att gaa tac atg caa aaa agg 590
Lys Lys His Glu Met Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg
                        160                        165                        170

gaa atc gag ctg caa aac gat aac atg tat ctc cgc tcc aag att act 638
Glu Ile Glu Leu Gln Asn Asp Asn Met Tyr Leu Arg Ser Lys Ile Thr
                        175                        180                        185

gaa aga aca ggt cta cag caa caa gaa tcg agt gtg ata cat caa ggg 686
Glu Arg Thr Gly Leu Gln Gln Gln Glu Ser Ser Val Ile His Gln Gly
                        190                        195                        200

aca gtt tac gag tcg ggt gtt act tct tct cac cag tcg ggg cag tat 734
Thr Val Tyr Glu Ser Gly Val Thr Ser Ser His Gln Ser Gly Gln Tyr
                        205                        210                        215

aac cgg aat tat att gcg gtt aac ctt ctt gaa ccg aat cag aat tcc 782
Asn Arg Asn Tyr Ile Ala Val Asn Leu Leu Glu Pro Asn Gln Asn Ser
220                        225                        230                        235

tcc aac caa gac caa cca cct ctg caa ctt gtt tga ttcagtctaa 828
Ser Asn Gln Asp Gln Pro Pro Leu Gln Leu Val
                        240                        245

cataagcttc tttcctcagc ctgagatcga tctatagtgt cacctaaatg cggccgcgtc 888

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 35 40 45
 Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile Phe Ser
 50 55 60
 Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr
 65 70 75 80
 Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro Pro Thr
 85 90 95
 Ile Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser Lys Leu
 100 105 110
 Arg Arg Gln Ile Arg Asp Ile Gln Asn Leu Asn Arg His Ile Leu Gly
 115 120 125
 Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu Glu Ser
 130 135 140
 Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys His Glu Met
 145 150 155 160
 Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Ile Glu Leu Gln
 165 170 175
 Asn Asp Asn Met Tyr Leu Arg Ser Lys Ile Thr Glu Arg Thr Gly Leu
 180 185 190
 Gln Gln Gln Glu Ser Ser Val Ile His Gln Gly Thr Val Tyr Glu Ser
 195 200 205
 Gly Val Thr Ser Ser His Gln Ser Gly Gln Tyr Asn Arg Asn Tyr Ile
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 Pro Pro Leu Gln Leu Val
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27

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 <213> Artificial Sequence

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<210> 11
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<220>
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<210> 12
<211> 18
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<210> 13
<211> 24
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<213> Artificial Sequence

<220>
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<210> 14
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<210> 15
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 <210> 17
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 amplification oligonucleotide primer

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 <210> 19
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<222> (2758)..(3354)

<223> R-like basic heix-loop-helix transcription factor
(R-like bHLH)

<400> 24

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 Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu
 35 40 45
 ctc aca caa gaa cac gca gct ttt ctc aat gat cct cac cat ctc atg 2949
 Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met
 50 55 60
 tta gat cca cct ccc gaa acc cta att cac ttg gac gaa gac gaa gag 2997
 Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu
 65 70 75 80
 tac gat gaa gac atg gat gcg atg aag gag atg cag tac atg atc gcc 3045
 Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala
 85 90 95

gtc atg cag ccc gta gac atc gac cct gcc acg gtc cct aag ccg aac 3093
 Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn
 100 105 110

cgc cgt aac gta agg ata agc gac gat cct cag acg gtg gtt gct cgt 3141
 Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg
 115 120 125

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 Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile
 130 135 140

gtg cct ggt ggt gcg aag atg gac aca gct tcc atg ctc gac gaa gcc 3237
 Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala
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 Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro
 165 170 175

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 His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys Tyr
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 Tyr His Asn Ser Gln Pro
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<213> Arabidopsis sp.

<400> 25

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 Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu
 35 40 45
 Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met
 50 55 60
 Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu
 65 70 75 80

[illegible]